DECLARATION AND POWER OF ATTORNEY FOR PATENT APPLICATION

Attorney Docket No. 5470-338

As a below named inventor, I hereby declare that:

My residence, post office address and citizenship are as stated below next to my name.

I believe I am the original, first and sole inventor (if only one name is listed below) or an original, first and joint inventor (if plural names are listed below) of the subject matter which is claimed and for which a patent is sought on the invention entitled REGULATION OF QUINOLATE PHOSPHORIBOSYL TRANSFERASE EXPRESSION,

the specification of which

☐ is attached hereto

OR

☒ was filed on 10 February 1998 as United States Application No. 09/021,286.

I hereby state that I have reviewed and understand the contents of the above-identified specification, including the claims, as amended by any amendment referred to above.

I acknowledge the duty to disclose information which is material to patentability as defined in Title 37 Code of Federal Regulations, §1.56.

I hereby claim foreign priority benefits under Title 35, United States Code, § 119(a)-(d) or § 365(b) of any foreign application(s) for patent or inventor's certificate, or § 365(a) of any PCT International application which designated at least one country other than the United States of America, listed below and have also identified below any foreign application for patent or inventor's certificate, or of any PCT International application having a filing date before that of the application on which priority is claimed.

NONE			☐ Yes ☐ No
Number	Country	MM/DD/YYYY Filed	Priority Claimed

I hereby claim the benefit under Title 35, United States Code, § 119(e) of any United States provisional application(s) listed below.

60/049,471	June 12, 1997
Application Number(s)	Filing Date (MM/DD/YYYY)

I hereby claim the benefit under Title 35, United States Code, § 120 of any United States application(s) or § 365(c) of any PCT international application designating the United States

of America, listed below and, insofar as the subject matter of each of the claims of this application is not disclosed in the prior United States or PCT International application(s) in the manner provided by the first paragraph of Title 35, United States Code, § 112, I acknowledge the duty to disclose information which is material to patentability as defined in Title 37, Code of Federal Regulations, § 1.56 which became available between the filing date of the prior application and the national or PCT international filing date of this application (37 C.F.R. § 1.63(d)).

None		
Appln. Serial No.	Filing Date	Status Patented/Pending/Abandoned

I hereby declare that all statements made herein of my own knowledge are true and that all statements made on information and belief are believed to be true; and further that these statements were made with the knowledge that willful false statements and the like so made are punishable by fine or imprisonment, or both, under Section 1001 of Title 18 of the United States Code and that such willful false statements may jeopardize the validity of the application or any patent issued thereon.

POWER OF ATTORNEY: As a named inventor, I hereby appoint the following registered attorney(s) to prosecute this application and transact all business in the Patent and Trademark Office connected therewith.

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Inventor's Signature: [signature] Date: 5/12/98

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Full name of second inventor: Wen Song

Inventor's Signature: ______________ Date: 5/12/98

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Full name of third inventor: Nandini Mendu

Inventor's Signature: Nandini Mendu Date: May 13, 1998

Residence: 5639 Chapel Hill Road, No. 207
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Citizenship: India

(A) NAME/KEY: CDS
(B) LOCATION: 52..1104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

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CAAAAACTAT TTTCCACAAA ATTCATTTCA CAACCCCCCC AAAAAAAAAC C ATG TTT      57
                                                          Met Phe
                                                            1

AGA GCT ATT CCT TTC ACT GCT ACA GTG CAT CCT TAT GCA ATT ACA GCT      105
Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile Thr Ala
          5                  10                  15

CCA AGG TTG GTG GTG AAA ATG TCA GCA ATA GCC ACC AAG AAT ACA AGA      153
Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn Thr Arg
     20                  25                  30

GTG GAG TCA TTA GAG GTG AAA CCA CCA GCA CAC CCA ACT TAT GAT TTA      201
Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr Asp Leu
 35                  40                  45                  50

AAG GAA GTT ATG AAA CTT GCA CTC TCT GAA GAT GCT GGG AAT TTA GGA      249
Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn Leu Gly
                 55                  60                  65

GAT GTG ACT TGT AAG GCG ACA ATT CCT CTT GAT ATG GAA TCC GAT GCT      297
Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser Asp Ala
             70                  75                  80

CAT TTT CTA GCA AAG GAA GAC GGG ATC ATA GCA GGA ATT GCA CTT GCT      345
His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala Leu Ala
         85                  90                  95

GAG ATG ATA TTC GCG GAA GTT GAT CCT TCA TTA AAG GTG GAG TGG TAT      393
Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu Trp Tyr
    100                 105                 110

GTA AAT GAT GGC GAT AAA GTT CAT AAA GGC TTG AAA TTT GGC AAA GTA      441
Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly Lys Val
115                 120                 125                 130

CAA GGA AAC GCT TAC AAC ATT GTT ATA GCT GAG AGG GTT GTT CTC AAT      489
Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val Leu Asn
                135                 140                 145

TTT ATG CAA AGA ATG AGT GGA ATA GCT ACA CTA ACT AAG GAA ATG GCA      537
Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu Met Ala
            150                 155                 160

GAT GCT GCA CAC CCT GCT TAC ATC TTG GAG ACT AGG AAA ACT GCT CCT      585
Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr Ala Pro
        165                 170                 175
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GGA TTA CGT TTG GTG GAT AAA TGG GCG GTA TTG ATC GGT GGG GGG AAG 633
Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly Gly Lys
180 185 190

AAT CAC AGA ATG GGC TTA TTT GAT ATG GTA ATG ATA AAA GAC AAT CAC 681
Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp Asn His
195 200 205 210

ATA TCT GCT GCT GGA GGT GTC GGC AAA GCT CTA AAA TCT GTG GAT CAG 729
Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val Asp Gln
215 220 225

TAT TTG GAG CAA AAT AAA CTT CAA ATA GGG GTT GAG GTT GAA ACC AGG 777
Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu Thr Arg
230 235 240

ACA ATT GAA GAA GTA CGT GAG GTT CTA GAC TAT GCA TCT CAA ACA AAG 825
Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln Thr Lys
245 250 255

ACT TCG TTG ACT AGG ATA ATG CTG GAC AAT ATG GTT GTT CCA TTA TCT 873
Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro Leu Ser
260 265 270

AAC GGA GAT ATT GAT GTA TCC ATG CTT AAG GAG GCT GTA GAA TTG ATC 921
Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu Leu Ile
275 280 285 290

AAT GGG AGG TTT GAT ACG GAG GCT TCA GGA AAT GTT ACC CTT GAA ACA 969
Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu Glu Thr
295 300 305

GTA CAC AAG ATT GGA CAA ACT GGT GTT ACC TAC ATT TCT AGT GGT GCC 1017
Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser Gly Ala
310 315 320

CTG ACG CAT TCC GTG AAA GCA CTT GAC ATT TCC CTG AAG ATC GAT ACA 1065
Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile Asp Thr
325 330 335

GAG CTC GCC CTT GAA GTT GGA AGG CGT ACA AAA CGA GCA TGAGCGCCAT 1114
Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
340 345 350

TACTTCTGCT ATAGGGTTGG AGTAAAAGCA GCTGAATAGC TGAAAGGTGC AAATAAGAAT 1174

CATTTTACTA GTTGTCAAAC AAAAGATCCT TCACTGTGTA ATCAAACAAA AAGATGTAAA 1234

TTGCTGGAAT ATCTCAGATG GCTCTTTTCC AACCTTATTG CTTGAGTTGG TAATTTCATT 1294

ATAGCTTTGT TTTCATGTTT CATGGAATTT GTTACAATGA AAATACTTGA TTTATAAGTT 1354

TGGTGTATGT AAAATTCTGT GTTACTTCAA ATATTTTGAG ATGTT 1399

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 351 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

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Met Phe Arg Ala Ile Pro Phe Thr Ala Thr Val His Pro Tyr Ala Ile
 1               5                  10                  15

Thr Ala Pro Arg Leu Val Val Lys Met Ser Ala Ile Ala Thr Lys Asn
            20                  25                  30

Thr Arg Val Glu Ser Leu Glu Val Lys Pro Pro Ala His Pro Thr Tyr
        35                  40                  45

Asp Leu Lys Glu Val Met Lys Leu Ala Leu Ser Glu Asp Ala Gly Asn
    50                  55                  60

Leu Gly Asp Val Thr Cys Lys Ala Thr Ile Pro Leu Asp Met Glu Ser
65                  70                  75                  80

Asp Ala His Phe Leu Ala Lys Glu Asp Gly Ile Ile Ala Gly Ile Ala
                85                  90                  95

Leu Ala Glu Met Ile Phe Ala Glu Val Asp Pro Ser Leu Lys Val Glu
            100                 105                 110

Trp Tyr Val Asn Asp Gly Asp Lys Val His Lys Gly Leu Lys Phe Gly
        115                 120                 125

Lys Val Gln Gly Asn Ala Tyr Asn Ile Val Ile Ala Glu Arg Val Val
    130                 135                 140

Leu Asn Phe Met Gln Arg Met Ser Gly Ile Ala Thr Leu Thr Lys Glu
145                 150                 155                 160

Met Ala Asp Ala Ala His Pro Ala Tyr Ile Leu Glu Thr Arg Lys Thr
                165                 170                 175

Ala Pro Gly Leu Arg Leu Val Asp Lys Trp Ala Val Leu Ile Gly Gly
            180                 185                 190

Gly Lys Asn His Arg Met Gly Leu Phe Asp Met Val Met Ile Lys Asp
        195                 200                 205

Asn His Ile Ser Ala Ala Gly Gly Val Gly Lys Ala Leu Lys Ser Val
    210                 215                 220

Asp Gln Tyr Leu Glu Gln Asn Lys Leu Gln Ile Gly Val Glu Val Glu
225                 230                 235                 240
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Thr Arg Thr Ile Glu Glu Val Arg Glu Val Leu Asp Tyr Ala Ser Gln
                245                 250                 255

Thr Lys Thr Ser Leu Thr Arg Ile Met Leu Asp Asn Met Val Val Pro
            260                 265                 270

Leu Ser Asn Gly Asp Ile Asp Val Ser Met Leu Lys Glu Ala Val Glu
        275                 280                 285

Leu Ile Asn Gly Arg Phe Asp Thr Glu Ala Ser Gly Asn Val Thr Leu
    290                 295                 300

Glu Thr Val His Lys Ile Gly Gln Thr Gly Val Thr Tyr Ile Ser Ser
305                 310                 315                 320

Gly Ala Leu Thr His Ser Val Lys Ala Leu Asp Ile Ser Leu Lys Ile
                325                 330                 335

Asp Thr Glu Leu Ala Leu Glu Val Gly Arg Arg Thr Lys Arg Ala
            340                 345                 350
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(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1053 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

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ATGTTTAGAG CTATTCCTTT CACTGCTACA GTGCATCCTT ATGCAATTAC AGCTCCAAGG      60
TTGGTGGTGA AAATGTCAGC AATAGCCACC AAGAATACAA GAGTGGAGTC ATTAGAGGTG     120
AAACCACCAG CACACCCAAC TTATGATTTA AAGGAAGTTA TGAAACTTGC ACTCTCTGAA     180
GATGCTGGGA ATTTTAGGAGA TGTGACTTGT AAGGCGACAA TTCCTCTTGA TATGGAATCC     240
GATGCTCATT TTCTAGCAAA GGAAGACGGG ATCATAGCAG GAATTGCACT TGCTGAGATG     300
ATATTCGCGG AAGTTGATCC TTCATTAAAG GTGGAGTGGT ATGTAAATGA TGGCGATAAA     360
GTTCATAAAG GCTTGAAATT TGGCAAAGTA CAAGGAAACG CTTACAACAT TGTTATAGCT     420
GAGAGGGTTG TTCTCAATTT TATGCAAAGA ATGAGTGGAA TAGCTACACT AACTAAGGAA     480
ATGGCAGATG CTGCACACCC TGCTTACATC TTGGAGACTA GGAAAACTGC TCCTGGATTA     540
CGTTTGGTGG ATAAATGGGC GGTATTGATC GGTGGGGGGA AGAATCACAG AATGGGCTTA     600
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